

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/517,079C  
Source: IFW  
Date Processed by STIC: 11/28/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

19517,079C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length      The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII      The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 ☐ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 ☐ Skipped Sequences  
    (OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for **each** skipped sequence:  
                                    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                    This sequence is intentionally skipped  
  
                                    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 ☐ Skipped Sequences  
    (NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                                    <210> sequence id number  
                                    <400> sequence id number  
                                    000
- 9 ☐ Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                                    Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                                    In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 ☐ Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>      Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n/Xaa      "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

DATE: 11/28/2006

PATENT APPLICATION: US/10/517,079C

TIME: 11:42:31

Input Set : N:\efs\11\_28\_06

\10517079c\_efs\Substitute\_Sequence\_Listing\_20747\_230.txt

Output Set: N:\CRF4\11282006\J517079C.raw

4 <110> APPLICANT: CePeP AB  
 6 <120> TITLE OF INVENTION: Cell Penetrating Peptides  
 9 <130> FILE REFERENCE: 20747/230  
 11 <140> CURRENT APPLICATION NUMBER: US 10/517,079C  
 C--> 12 <141> CURRENT FILING DATE: 2004-12-06  
 14 <150> PRIOR APPLICATION NUMBER: PCT/IB03/03163  
 15 <151> PRIOR FILING DATE: 2003-06-18  
 17 <150> PRIOR APPLICATION NUMBER: US 60/391,788  
 18 <151> PRIOR FILING DATE: 2002-06-25  
 20 <150> PRIOR APPLICATION NUMBER: SE 0201863-8  
 21 <151> PRIOR FILING DATE: 2002-06-18  
 23 <160> NUMBER OF SEQ ID NOS: 31933  
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0

## ERRORED SEQUENCES

Does Not Comply  
 Corrected Diskette Needed

(pg.1-6)

38551 <210> SEQ ID NO: 2739  
 38552 <211> LENGTH: 16  
 38553 <212> TYPE: PRT  
 38554 <213> ORGANISM: Homo Sapiens  
 38556 <220> FEATURE:  
 38557 <222> LOCATION: ( 259 )...( 275 )  
 38558 <223> OTHER INFORMATION: 5H6\_HUMAN  
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 38560 His Ser Arg Lys Ala Leu Lys Ala Ser Leu Thr Leu Gly Ile Leu Leu  
 E--> 38561 1 5 10 15  
 38565 <210> SEQ ID NO: 2740  
 38566 <211> LENGTH: 16  
 38567 <212> TYPE: PRT  
 38568 <213> ORGANISM: Homo Sapiens  
 38570 <220> FEATURE:  
 38571 <222> LOCATION: ( 260 )...( 276 )  
 38572 <223> OTHER INFORMATION: 5H6\_HUMAN  
 W--> 38573 <400> SEQUENCE: 2740  
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 E--> 38575 1 5 10 15  
 38579 <210> SEQ ID NO: 2741  
 38580 <211> LENGTH: 16  
 38581 <212> TYPE: PRT  
 38582 <213> ORGANISM: Homo Sapiens  
 38584 <220> FEATURE:  
 38585 <222> LOCATION: ( 261 )...( 277 )

See  
 item  
 #3 on  
 error  
 summary  
 sheet.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/517,079C

DATE: 11/28/2006  
TIME: 11:42:33

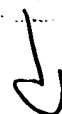
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\10517079c\_efs\Substitute\_Sequence\_Listing\_20747\_230.txt

Output Set: N:\CRF4\11282006\J517079C.raw

38586 <223> OTHER INFORMATION: 5H6\_HUMAN  
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E--> 38589 1 5 10 15  
38593 <210> SEQ ID NO: 2742  
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38595 <212> TYPE: PRT  
38596 <213> ORGANISM: Homo Sapiens  
38598 <220> FEATURE:  
38599 <222> LOCATION: ( 108 )...( 124 )  
38600 <223> OTHER INFORMATION: 5H7\_HUMAN  
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38602 Phe Val Lys Lys Leu Arg Gln Pro Ser Asn Tyr Leu Ile Val Ser Leu  
E--> 38603 1 5 10 15  
38607 <210> SEQ ID NO: 2743  
38608 <211> LENGTH: 16  
38609 <212> TYPE: PRT  
38610 <213> ORGANISM: Homo Sapiens  
38612 <220> FEATURE:  
38613 <222> LOCATION: ( 109 )...( 125 )  
38614 <223> OTHER INFORMATION: 5H7\_HUMAN  
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38621 <210> SEQ ID NO: 2744  
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38623 <212> TYPE: PRT  
38624 <213> ORGANISM: Homo Sapiens  
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38627 <222> LOCATION: ( 110 )...( 126 )  
38628 <223> OTHER INFORMATION: 5H7\_HUMAN  
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38641 <222> LOCATION: ( 305 )...( 321 )  
38642 <223> OTHER INFORMATION: 5H7\_HUMAN  
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38644 Leu Ser Arg Leu Leu Lys His Glu Arg Lys Asn Ile Ser Ile Phe Lys  
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38649 <210> SEQ ID NO: 2746  
38650 <211> LENGTH: 16  
38651 <212> TYPE: PRT  
38652 <213> ORGANISM: Homo Sapiens  
38654 <220> FEATURE:

Same  
errors



See

item #3

on error

Summary

Sheet

## RAW SEQUENCE LISTING

DATE: 11/28/2006

PATENT APPLICATION: US/10/517,079C

TIME: 11:42:33

Input Set : N:\efs\11\_28\_06

\10517079c\_efs\Substitute\_Sequence\_Listing\_20747\_230.txt

Output Set: N:\CRF4\11282006\J517079C.raw

38655 <222> LOCATION: ( 248 )...( 264 )  
38656 <223> OTHER INFORMATION: A1AA\_HUMAN  
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38658 Met Ala Ser Ala Lys Thr Lys Thr His Phe Ser Val Arg Leu Leu Lys  
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38664 <211> LENGTH: 16  
38665 <212> TYPE: PRT  
38666 <213> ORGANISM: Homo Sapiens  
38668 <220> FEATURE:  
38669 <222> LOCATION: ( 261 )...( 277 )  
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38683 <222> LOCATION: ( 262 )...( 278 )  
38684 <223> OTHER INFORMATION: A1AA\_HUMAN  
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E--> 38687 1 5 10 15  
38691 <210> SEQ ID NO: 2749  
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38693 <212> TYPE: PRT  
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38697 <222> LOCATION: ( 268 )...( 284 )  
38698 <223> OTHER INFORMATION: A1AA\_HUMAN  
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38705 <210> SEQ ID NO: 2750  
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38708 <213> ORGANISM: Homo Sapiens  
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38711 <222> LOCATION: ( 151 )...( 167 )  
38712 <223> OTHER INFORMATION: A1AB\_HUMAN  
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E--> 38715 1 5 10 15  
38719 <210> SEQ ID NO: 2751  
38720 <211> LENGTH: 16  
38721 <212> TYPE: PRT  
38722 <213> ORGANISM: Homo Sapiens

Same  
errors

See item

#3 on

error

Summary

Sheet

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/517,079C

DATE: 11/28/2006  
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Input Set : N:\efs\11\_28\_06

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Output Set: N:\CRF4\11282006\J517079C.raw

38724 <220> FEATURE:  
38725 <222> LOCATION: ( 152 )...( 168 )  
38726 <223> OTHER INFORMATION: A1AB\_HUMAN  
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38733 <210> SEQ ID NO: 2752  
38734 <211> LENGTH: 16  
38735 <212> TYPE: PRT  
38736 <213> ORGANISM: Homo Sapiens  
38738 <220> FEATURE:  
38739 <222> LOCATION: ( 154 )...( 170 )  
38740 <223> OTHER INFORMATION: A1AB\_HUMAN  
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E--> 38743 1 5 10 15  
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38753 <222> LOCATION: ( 155 )...( 171 )  
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38768 <223> OTHER INFORMATION: A1AB\_HUMAN  
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E--> 38771 1 5 10 15  
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38789 <210> SEQ ID NO: 2756  
38790 <211> LENGTH: 16  
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Same  
errors

## RAW SEQUENCE LISTING

DATE: 11/28/2006

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Input Set : N:\efs\11\_28\_06

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Output Set: N:\CRF4\11282006\J517079C.raw

38792 <213> ORGANISM: Homo Sapiens  
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38795 <222> LOCATION: ( 158 )...( 174 )  
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38824 <223> OTHER INFORMATION: A1AB\_HUMAN  
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E--> 38827 1 5 10 15  
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E--> 38855 1 5 10 15  
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38860 <211> LENGTH: 16

Same  
errorsSee item  
#3 on  
error  
summary  
sheet

## RAW SEQUENCE LISTING

DATE: 11/28/2006

PATENT APPLICATION: US/10/517,079C

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Input Set : N:\efs\11\_28\_06

\10517079c\_efs\Substitute\_Sequence\_Listing\_20747\_230.txt

Output Set: N:\CRF4\11282006\J517079C.raw

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38904 <213> ORGANISM: Homo Sapiens  
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38915 <210> SEQ ID NO: 2765  
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38918 <213> ORGANISM: Homo Sapiens  
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38921 <222> LOCATION: ( 338 )...( 354 )  
38922 <223> OTHER INFORMATION: A1AD\_HUMAN  
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E--> 38925 1 5 10 15  
38929 <210> SEQ ID NO: 2766

Same  
errors

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.